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OM protein - protein search, using sw model		Run on: December 27, 2001, 16:52:25 ; Search time 16.97 Seconds	
Sequence: US-09-830-647-1		(without alignments) 1456.222 Million cell updates/sec	
Perfect score: 3510		Post-processing: Minimum Match 0%	
Scoring table: BLOSUM62		Maximum DB seq length: 0	
Searched: Gapop 10.0 , Gapext 0.5		Maximum DB seq length: 200000000	
total number of hits satisfying chosen parameters: 100059		Post-processing: Minimum Match 100%	
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		Listing first 45 summaries	
Database : SwissProt 39:*		SUMMARIES	
Result No.		% Query	
Score		Match length	
Match ID		DB ID	
Description		Description	
No.		No.	
187		187	
5.3		5.3	
1790		1790	
1		1	
USOL_YEAST		USOL_YEAST	
P25386; saccharomyces cerevisiae (Baker's Yeast)		STANDARD; PRT: 1790 AA.	
0.9996		0.9996	
h a kinase		h a kinase	
0.92184		0.92184	
gallus gallus		gallus gallus	
0.13439		0.13439	
homo sapien		homo sapien	
P30622		P30622	
homo sapien		homo sapien	
P49454		P49454	
homo sapien		homo sapien	
P53914		P53914	
saccharomyces cerevisiae (Baker's Yeast)		saccharomyces cerevisiae (Baker's Yeast)	
0.02244		0.02244	
homo sapien		homo sapien	
Q9ng66		Q9ng66	
homo sapien		homo sapien	
P27573		P27573	
saccharomyces cerevisiae (Baker's Yeast)		saccharomyces cerevisiae (Baker's Yeast)	
0.63358		0.63358	
ratmus norvegicus		ratmus norvegicus	
Q09857		Q09857	
schizosaccharomyces pombe		schizosaccharomyces pombe	
Q14157		Q14157	
schizosaccharomyces pombe		schizosaccharomyces pombe	
P04934		P04934	
plasmid		plasmid	
P5045		P5045	
plasmid		plasmid	
P54697		P54697	
dictyosteliellaceae		dictyosteliellaceae	
P41003		P41003	
schizosaccharomyces pombe		schizosaccharomyces pombe	
P47460		P47460	
mycoplasma		mycoplasma	
Q9qy06		Q9qy06	
mus musculus		mus musculus	
P02455		P02455	
saccharomyces cerevisiae (Baker's Yeast)		saccharomyces cerevisiae (Baker's Yeast)	
P48582		P48582	
saccharomyces cerevisiae (Baker's Yeast)		saccharomyces cerevisiae (Baker's Yeast)	
P10587		P10587	
galinus gallus		galinus gallus	
Q10411		Q10411	
schizosaccharomyces pombe		schizosaccharomyces pombe	
P10687		P10687	
ratmus norvegicus		ratmus norvegicus	
P29374		P29374	
homo sapien		homo sapien	
Q49419		Q49419	
mycoplasma		mycoplasma	
P04932		P04932	
plasmid		plasmid	
P04933		P04933	
plasmid		plasmid	
P04934		P04934	
strongylidae		strongylidae	
P23908		P23908	
saccharomyces cerevisiae (Baker's Yeast)		saccharomyces cerevisiae (Baker's Yeast)	
P250357		P250357	
saccharomyces cerevisiae (Baker's Yeast)		saccharomyces cerevisiae (Baker's Yeast)	
P049429		P049429	
mycoplasma		mycoplasma	
P200_MCGE		P200_MCGE	

KW Transport; Protein transport; Golgi stack; Cytoskeleton; Coiled coil.
 FT DOMAIN 1 724 GLOBULAR HEAD.
 FT DOMAIN 725 1790 COILED COIL (POTENTIAL).
 FT DOMAIN 465 487 CHARGED (HYPER-HYDROPHILIC).
 FT DOMAIN 991 1790 DISPENSABLE FOR THE PROTEIN FUNCTION.
 FT CONFLICT 1172 1786 ASP/GLU-RICH (ACIDIC).
 FT CONFLICT 847 947 G > E (IN REF. 2).
 FT CONFLICT 924 924 E -> K (IN REF. 2).
 FT CONFLICT 1253 1253 V -> I (IN REF. 2).
 FT CONFLICT 1319 1319 I -> V (IN REF. 2).
 FT CONFLICT 1461 1461 N -> S (IN REF. 2).
 FT CONFLICT 1581 1581 G -> S (IN REF. 2).
 FT CONFLICT 1600 1600 I -> V (IN REF. 2).
 FT CONFLICT 1661 1661 R -> S (IN REF. 2).
 FT CONFLICT 1772 1772 D -> DEDDDE (IN REF. 2).
 SQ SEQUENCE 1790 AA; 206424 MW; 6CE2B216E9FD4818 CRC64;

Query Match 5.3%; Score 187; DB 1; Length 1790;
 Best Local Similarity 19.9%; Pred. No. 0.016;
 Matchers 150; Conservative 133; Mismatches 273; Indels 198; Gaps 31;

QY 2 NSGAMRIRHKHFGQIGIQVNEKNRPSLKIQTDRNPRERSKRCKPLWGKVFVYDLPSTV 61
 Db 978 NESLIKAVESKNNSNLSNLQNKDMSQEN-----RQEJESIEK 1023
 QY 62 -EKLOQDKIOLGGVEELSK-----DISLISKWKEAFA-QTGRLSIVPSP 108
 Db 1024 1EQQLKTTISDLEQKREELSKPSBSSKDEYEQSQISLUKELETATTAENDENYKISBLKT 1083
 QY 109 ESEAYTETPSPHPSHDGGSFKSPDTVLSRGKLVYEAKDHDHIPSINSIANSWGV 168
 Db 1084 REELEAELAA-----YKLNKNELEKLETS--EKAKE--VKEE----- 1119
 QY 169 IHLDDIDRYYTEQK---KKEYLKKKSSTSVRDGGKRVGSGAQKTRGRKKPFEVED 224
 Db 1120 -EHLKEKIKOLEKATEKTKOOLNLSRNLANSLESKHEHDLAQKYYEQIANKERYNE 1178
 QY 225 MSQLYRPFYQLTNMPFINYSTQKPCSPFDV --KPPSMQKOTQVKLRLTGDKYGGT 281
 Db 1179 ISQNLND---EITSQOENESTIKKNDLVEGEVKAMKSTSEOSNLK-KS1D----- 1226
 QY 282 SIQLOQIKEKKKGVC-----ECQKYE--DILETHISEQH 315
 Db 1227 ALNQIKELKKKNETNEAASSLSESIKSVESTVTKELQDCECNKEKEVSELEDKLASED 1286
 QY 316 RNF---AQNOQYQVVDIVSKLVEFVEKEKDPEKKRKYVGSIISPVAVSKVTEO 371
 Db 1287 KNSKYLELQKSEKEIQLDKEVTEKLQIQLKETITNLSKAKKESELSR---LKKTS 1341
 QY 372 KERVELQHISQKDCQEDDTVKEQNFYKETQETEKKL---F1SEPIRHPNBLRGL 426
 Db 1342 EER-----KNAEOLKEKNEIQLKNAQAFERKEKRLINEGSSITQEQYKINTLE 1393
 QY 427 NEKMSKCKSMIQAEDDTIQNTOLPLH---KRNQECILDSEHTL----- 470
 Db 1394 LIRLQNELEKAKEDINTNRELEKVLNSNDBLEKONTIKSLODETLSYKDKITRDER 1453
 QY 471 -----ENDLEPLR---VDHYKNCQ-----ASV 490
 Db 1454 LISTERDNKRDLESLKQRAQAEQSKAVKREGKLEESKRAELEKSEMMRLEST 1513
 QY 491 HVSDESTDHSQSPKQPKDVTFLPKDLDKLQDLSIFTHDSGLT-NSSCB-----H 542
 Db 1514 IESNETELKSSMEIRKSDKELEQSKSAEEDIRNLQHEKSDLSRNESEKDBELSK 1573
 QY 543 LTVQK -APFHTPPEEDENCODFKNMDSLPSGK-HRKYKILGMRNRLNLPNAFEDKRT 600
 QY 1574 LRIEAKSGSELETVQKELNAQEKI-----RINAENTVVL-KSKLDEDIERELK-DKQA 1624
 Db 601 EF-TQENRICSSPVQSLL-LDIFQTSEKSE 630
 QY 1625 EIKSNQEBERKLTSRLEQELDSTQOKAQSE 1658

RESULT 2
 ID AKA9_HUMAN
 ID AKA9_HUMAN STANDARD: PRT; 3911 AA.
 ID Q99956; Q9UQ04; Q9UH3; Q9Y6Y2; O14859; 043355; Q9Y6BB;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE A KINASE ANCHOR PROTEIN 9 (PROTEIN KINASE A ANCHORING PROTEIN 9)
 DE (PRAK9) (A-KINASE ANCHOR PROTEIN 450 KDa) (AKAP 450) (A-KINASE ANCHOR PROTEIN 350 KDa) (AKAP 350) (HAKAP 350) (AKAP 120 like protein) (HYPERION PROTEIN) (NOTILO) (CENTROZONE- AND GOLGI-LOCALIZED PKN ASSOCIATED PROTEIN) (CG-NAP).
 DE AKAP9 OR AKAP450 OR AKAP350 OR KIAA083.
 OS Homo sapiens (Human).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBIL-TAXID=9606;
 OX [1];
 RN N
 RP SEQUENCE FROM N.A. (ISOFORM 4).
 RC TISSUE=Brain;
 RC MEDLINE=98151389; PubMed=9482789;
 RA Lin J.W., Wyszynski M., Madhavan R., Sealock R., Kim J.U., Sheng M.;
 RA "Yotiao, a novel protein of neuromuscular junction and brain that interacts with specific splice variants of NMDA receptor subunit NR1,"
 RA J. Neurosci. 18:2017-2027(1998).
 RA [2];
 RA Witczak O., Skalhegg S., Keryer G., Bornens M., Tasken K.,
 RA J. Neurosci. 18:2017-2027(1998).
 RA [3];
 RA Tissue-Brain;
 RA MEDLINE=99219864; PubMed=10202199;
 RA RUL PROTEIN; RNL EMB0 J. 18:1858-1868(1999).
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC Tissue-Brain;
 RA "Cloning and characterization of a cDNA encoding an A-kinase anchoring protein located in the centrosome, AKAP450."
 RA RUL PROTEIN; RNL EMB0 J. 18:1858-1868(1999).
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Kemmer W.A., Deiss S., Schwarz U.;
 RT "Cloning of Hyperion.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
 RN [5];
 RP SEQUENCE OF 323-3911 FROM N.A. (ISOFORM 2).
 RC TISSUE=Gastric parietal cell;
 RX MEDLINE=99115634; PubMed=9915845;
 RA Schmidt P.H., Dransfield D.T., Claudio J.O., Hawley R.G.,
 RA Trotter K.W., Milgram S.I., Goldring J.R.,
 RT "AKAP350, a multiply spliced protein kinase A-anchoring protein associated with centrosomes."
 RL J. Biol. Chem. 274:2055-3066(1999).
 RN [6];
 RP SEQUENCE OF 1807-3876 FROM N.A. (ISOFORM 5).
 RC TISSUE="lymphoblast";
 RA Hinds K., Sutteer C., Becker M., Hawkins M.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
 RN [7];
 RP SEQUENCE OF 2157-3911 FROM N.A. (ISOFORM 6).
 RC TISSUE="lung";
 RA Milgram S.L., Goldring J.R., Schmidt P.H.;
 RT "AKAP350: A multiply spliced family of proteins with centrosomal association.";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
 RN [8];
 RP SEQUENCE OF 2212-3911 FROM N.A. (ISOFORM 2/3).

- I - SIMILARITY: TO S. POMBE SPAC20G8.09C AND AN A. AMBISEXUALIS HYPOTHETICAL PROTEIN (AC P54008).

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CC EMBL: 246843; CAAB893_1; DR SGD: 5005016; YNL32W.

KW HYPOTHETICAL PROTEIN; ATP-BINDING.

FT NP-BIND 283 290 ATP (POTENTIAL).

SQ SEQUENCE 1056 AA; 119347 MW; 76721ED0867ED618 CRC64;

Query Match 4 4%; Score 155.5; DB 1; Length 1056; Best Local Similarity 21.0%; Pred. No. 0.37; Mismatches 235; Indels 235; Gaps 37; Matches 151; Conservative 98; MisMatches 235; InDels 235; Gaps 37;

QY 19 QVNEKNEKPKSLKLT---DNRPEPKSKCKPLWGVFYIDLPVYISE-KLQDKDIL- 71

Db 429 QLNQNNTNGESTQTAWSRDKEKOS-----HHSQQRQLRBTISDEPIVAP 478

QY 72 GGRVEERLSKQISYLSINKEAKA-----QQLGRISPVPS----- 107

Db 479 GDPIEKWNKLNUCLDVTLKNPRAFTQTPHPSQCNLFVNNRDTFSYHPVSENLEKMM 538

QY 108 -----PESAVTETTSPHPS-----DGSSPKSDPTVC----- 135

Db 539 ALVYSSHKKNSPNDLQIMSDAPKLFVFLPVIDPKGG---RIPOLPCVITALEGEISK 596

QY 136 -----LGRK-----LLVERAIKHDHFPSNS---ILSN---ALSGVKTHTI 172

Db 597 ESRNLSLSRGQRAGGDLIPWHLISQOFQDEFASFSLSGARIVRATNPVEASMGGSRAEL 656

QY 173 DDTRYVYBOKKELYLKKSSTSVDGG---KRVGSAQKRTGRLKPKFVKVQEDMSQY 229

Db 657 -LIRDYFEGKFDM---SEDRPKYKSIKV-SDKELAKTNLKDD-VKLRAKTL- 705

QY 230 RPYPLQIINMP-----FINISYQKCPSPFDVKQSSMOKQTOQKLQDODKYG-GT 281

Db 706 PPLIKLSEQPHYLGYLSQNSKFK-WKNSF--VPMYLRTQADLTCET 759

QY 282 SIQLQLEKKKKGYCECCQKYEDETHLISFQHNRFAQSNQYQVDDIVSKLFDFVEY 341

Db 760 CVMVLNLBGRSNNWLVEFAKDFRKRFLSLSYDFHKTAVDALSIES-SKRAQDLSSD 817

QY 342 EKOPPK-----KAI-KS-----VGSPSPYASVVIKTKTQKVEL 377

Db 818 EKHDKELTRHLDIFSPFDLKKRIDSYSNNLDHYVIGMIPMALLFGDKMGDSKL 877

QY 378 QHISQK-----DCEQDVTQKQNFYKETQETEKKLIFSEPIPHPSNEURGLNEKM 430

Db 878 SSVQSATLAIQKRNNTDIAKEINL-----PSNOTIAMPKI 916

QY 431 SNKCSMUSTAEDDIRNFTDPLKHKNCUCLDISETSLNDLFLRLDHYKNCIASV 490

Db 917 MRKMS-----QYFROL-LSQSIEETLPKIDDAEMDGEIK----NYNAE 959

QY 491 HVSDFSTD-NSGQPKQKSDTIVLEPAKDLKEDKUDHSITFHDGSLTNS---SDEHL 543

Db 960 ALDPMEEELERAGESEAVQ-----AMKEQKBLINSLNIDKYLINDSEWEAEQSL 1011

QY 544 TVQKAPFHTPPEEPNECDFKNMDSLPSCK-----LHRKVKILLGRNRKENLEP 593

Db 1012 EIAKA-----KGWVSLKIGKRTTEKAEDIYRQEMKAMKPRSKKAAN 1056

CC CENE_HUMAN STANDARD; PRT; 2663 AA.

ID CENE_HUMAN ID CENE_HUMAN

AC 00224; DT 01-JUL-1993 (Rel. 26, Created)

DR 01-JUL-1993 (Rel. 26, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE CENTROMERIC PROTEIN E (CENP-E PROTEIN).

GN CENE.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI-TaxID=9606;

OX RN [1] SEQUENCE FROM N.A.

RP MEDLINE-9302922; PubMed-1406971;

RX RA Yen T.J., Li B.T., Schaar B.T., Sziaki I., Cleveland D.W.; just before mitosis.

RT "CENP-E is a putative kinetochore motor that accumulates before mitosis."

RL Nature 359:536-539(1992).

RN [2] CHARACTERIZATION.

RP MEDLINE-95196755; PubMed-9789940;

RX MEDLINE-98437347; PubMed-9763420;

RA Chan G.K.T., Jordan M.A., Schaar B.T., Yen T.J., Wilson L.; Thrower D.A., Jordan M.A., Schaar B.T., Yen T.J., Wilson L.;

RT "Mitotic HeLa cells contain a CENP-E-associated minus end-directed microtubule motor."

RT Interactions with the kinetochore proteins CENP-F and hBUBR1.";

RL EMBL: 14:918-926(1995).

CC [3] CHARACTERIZATION.

CC MEDLINE-98437347; PubMed-9763420;

CC Chan G.K.T., Schaar B.T., Yen T.J., Wilson L.; Thrower D.A., Jordan M.A., Schaar B.T., Yen T.J., Wilson L.;

CC "Characterization of the kinetochore binding domain of CENP-E reveals interactions with the kinetochore proteins CENP-F and hBUBR1.";

CC J. Cell Biol. 143:49-63(1998).

CC [4] FUNCTION: MINUS-END DIRECTED MICROTUBULE MOTOR. PROBABLE KINETOCHEMOTOR. ACCUMULATES JUST BEFORE MITOSIS AT THE G2 PHASE OF THE CELL CYCLE. PROBABLY IMPORTANT FOR CHROMOSOME MOVEMENT AND/OR SPINDLE ELONGATION.

CC [5] SUBUNIT: INTERACTS WITH CENP-F AND BUBR1 KINASE.

CC [6] SUBCELLULAR LOCATION: ASSOCIATES WITH KINETOCHORES DURING CONGREGATION, RELOCATES TO THE SPINDLE MIDZONE AT ANAPHASE, AND IS QUANTITATIVELY DISCARDED AT THE END OF THE CELL DIVISION.

CC [7] SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.

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CC EMBL: 210005; CAAB893_1; DR PIR: S28261; S28261.

DR HSSP: P01069; IZII.

DR MIM: 17143; DR Interpro; IPR01752; kinesin.

DR Pfam: PF00225; kinesin; 1.

DR PRINTS: PR00310; KINESIN-HEAVY.

DR SMART: SM01219; KISC; 1.

DR PROSITE; PS00411; KINESIN_MOTOR_DOMAIN; 1.

DR PROSITE; PS0067; KINESIN_MOTOR_DOMAIN; 1.

DR Motor protein; Cell division; ATP-binding; Coiled coil; Mitosis; Cell cycle; Centromere.

FT DOMAIN 1 335

FT DOMAIN 336 2471

FT DOMAIN 2472 2663

FT NP-BIND 86 93 ATP (BY SIMILARITY).

SQ SEQUENCE 2663 AA; 312087 MW; CFC13880C8C8CB8 CRC64;

Query Match 4 4%; Score 154; DB 1; Length 2663; Best Local Similarity 18.2%; Pred. No. 1.5; Mismatches 243; Indels 300; Gaps 37; Matches 147; Conservative 117; MisMatches 243; InDels 300; Gaps 37;

QY 18 TVKNEKNRPSLUSKLKDNR-----PEKSKCKPLMGKVFYDLPSPVTESEKLODKD 72
 RP SEQUENCE FROM N.A. (ISOFORMS A AND B).
 RC TISSUE=Brain;
 RX Published=11118617;
 RA Caricasole A., Sala C., Roncarati R., Fermenti E., Terstappen G.C.;
 RT "Cloning and characterization of the human phosphoinositide-specific
 phospholipase C-beta 1 (PLCbeta1)";
 RT Biochim. Biophys. Acta 1517:63-72(2000).
 RN [2]
 QY 1438 -----KSWAKEKDOLQRQEVLOQESFDQKENI----- 1465
 RP SEQUENCE FROM N.A. (ISOFORM A).
 RC TISSUE=Brain;
 RX MEDLINE=20225428; PubMed=10760467;
 RA PERUZZI D., CALABRESE G., FAENZA I., MANZOLI L., MATTEUCCI A.,
 RA GIANFRANCESCO F., BILLI A.M., STUPPIA L., PALKA G., COCCO L.;
 RT Identification and chromosomal localisation by fluorescence in situ
 hybridisation of human gene of phosphoinositide-specific phospholipase
 C beta 1.";
 RT Biochim. Biophys. Acta 1484:175-182(2000).
 RN [3]
 QY 1466 -----KETIVAKHLETEE----- 1504
 RP SEQUENCE OF 261-1216 FROM N.A. (ISOFORM B).
 RA ISSUE=Fastis;
 RA KOEHR K., BEYER A., MEWES H.-W., GASSENHUBER J., WLEMMANN S.;
 RA Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 DB 1505 TEISTIQKOLEAINDKLQNQKIQEYKEEQDNIQKQSEWQENNEKLQFKEHRKAKOSA 1564
 RA 1619 KMKEQSKPQFPLKMTAVNEQEKMCETEHLK-EQFETQKUNIENIETENRILQTHEN 1677
 RA SEQUENCE OF 519-1216 FROM N.A. (ISOFORM A).
 TISSUE=Brain;
 RX MEDLINE=982290545; PubMed=9629581;
 RA NARASE T., ISHIKAWA K.-I., MIYAJIMA N., TANAKA A., KOTANI H.,
 RA NOMURA N., OHARA O.;
 RT "Prediction of the coding sequences of unidentified human genes. IX.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro.";
 RL DNA Res. 5:31-39(1998).
 CC -1- FUNCTION: THE PRODUCTION OF THE SECOND MESSENGER MOLECULES
 CC DIACYLGLYCEROL (DAG) AND INOSITOL 1,4,5-TRIPHOSPHATE (IP3) IS
 CC MEDIANED BY ACTIVATED PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
 CC C ENZYMES.
 CC -1- CATALYTIC ACTIVITY: 1-PHOSPHATIDYL-D-MYO-INOSITOL 4,5-BISPHOSPHATE
 CC + H2O = D-MYO-INOSITOL 1,4,5-TRIPHOSPHATE + DIACYLGLYCEROL.
 CC -1- COFACTOR: REQUIRES CALCIUM.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE), AND B; ARE
 CC PRODUCED BY ALTERNATIVE SPlicing.
 CC -1- MISCELLANEOUS: THE RECEPTOR-MEDIATED ACTIVATION OF PLC-BETA 1 IS
 CC MEDIATED BY TWO G-PROTEIN ALPHA SUBUNITS, ALPHA-Q AND ALPHA-11.
 CC -1- SIMILARITY: DOMAINS X AND Y ARE CONSERVED IN DIFFERENT FORMS
 CC OF PLC AND ARE ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -1- SIMILARITY: CONTAINS 1 C2 DOMAIN.
 CC
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 CC
 DB 1725 IVHMHKERQEDIDKLRGIVSPTNEISMQDLEHNDALKDQKEDQEEHLRAHHLK 1784
 CC
 QY 401 ETQETEKKLL-FISEP1PHPSN--ELRGNEKMSNKS-----MLSTAEDDIQ--- 446
 CC
 DB 1785 EQETIDKLRGIVSEKTDKLSNMQDLENSNAKQELKANEHOLITLKDVNTEQK 1844
 CC
 QY 447 -----NFTQPLHKKQEC----- 171
 CC
 DB 1845 KVSEMEQOLKQIKDQSLTSLKLEIENNLQ-ELHENLEMKVSKMVKERDNLRRVEEDL 1903
 CC
 QY 465 SEHTLSN-----DLE---ELR----- 17
 CC
 DB 1904 ERDQKLESQETKAROLEIQEPLKTPAMSKHEKETVDRKLERKISERTQISDIOKLDK 1963
 CC
 QY 502 SQPKQKSDTVPKDLKJKEKDHSGLITINSQEHLT--VQAKAPHTPPLEPN 559
 CC
 DB 1964 SK-----DELORKQILOQKELQKELQRLYKED---VNNHKKINEMEOLKKOF---EPN 2009
 CC
 QY 560 --ECDPKNMNLSPLPSKIH--RKVKTLL---RNRKNEPLNAEFDKRFEPF1---- 603
 CC
 DB 2010 YICKCERADNFQL-TKXHESLEERIVAKERDELRLRIKESKM-----ERDQFIATLRE 2062
 CC
 QY 604 -----TOEENRICSSPVQOSLID 620
 CC
 DB 2063 MARDRDNHQVKEPKRLLSDQOHLME 2089
 CC
 RESULT 9
 PBL1_HUMAN
 PBL1_HUMAN STANDARD; PRT; 1216 AA.
 AC Q9NQ66; Q9NQH9; Q9NPH4; 060325;
 DT 20-AUG-2001 (rel. 40, Created)
 DT 20-AUG-2001 (rel. 40, Last sequence update)
 DT 20-AUG-2001 (rel. 40, Last annotation update)
 DE 1-PHOSPHATIDYLINOSITOL-4',5'-BISPHOSPHATE PHOSPHODIESTERASE BETA 1
 DE (EC 3.1.4.11) (PLC-BETA-1) (PHOSPHOLIPASE C-BETA-1) (PLC-1) (PLC-154).
 DE GN OR KITA0581.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Cetartiodactyla; Hominidae; Homo.
 OC NCBI_TaxID:9606;
 LN [1]

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONES TO THE VDP/USON/YB047C FAMILY.
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 CC or send an email to license@ib-sib.ch).
 CC
 DR EMBL; 26652; CAA91425.1; ALT_SEQ.
 DR EMBL; ALI3653; CAB6666.; -.
 KW Hypothetical protein; Coiled coil.
 FT DOMAIN 600 1014 COILED COIL (POTENTIAL).
 SQ SEQUENCE 104 AA; 119127 MW; 52ACED174725A59 CRC64;

Query Match 4.3%; Score 151.5; DB 1; Length 1044;
 Best Local Similarity 19.5%; Pred. No. 0.6; DB 1; Length 1044;
 Matches 130; Conservative 122; Mismatches 214; Gaps 34;
 QY 52 YLDIPSVTISEKIQDKIDKLGGRVEFLSKDISLNKEAKFAOTLGRISPVSPBSA 111
 Db 418 YLDL--VHLDSDQDY---IQCVST--KLIATLRRHANLNCVGLTLLALVYGNPDS 514
 QY 112 YTAETTSPIPSHDGSSSKSPPTVCLSRGKLV---EKAID--
 Db 463 DNDEDSE--SEDKVTF---IQCVST--KLIATLRRHANLNCVGLTLLALVYGNPDS 514
 QY 150 -HDEPISNIL--
 Db 515 VKDTESESSILQFLTALMDESSANSVQGMAYFLWVYCPESPVSKSYV--- 570
 QY 192 SSTSVRDGKRVGSAQRTGRGLRKPFVWEDMSOLQYRFLQUNMPFTINYSTQPCS 251
 Db 571 -----NATSAVRD--VETNRLRUR--MNLVETFL----- 600
 QY 252 PFDVDPKSSPMQKOTQVK-LRQTDGSKYGTTSQIQLKE-----KKKGYCBC 298
 Db 601 -----SMOKMQLSKREIDNPK--EALDSYKERSIOEKLNESTKTSRNLEE 649
 QY 299 CLQRYEDLETHLSEODR-----NPAQSN-----OYQVDDIVSKVLFDEV-EYEV 343
 Db 650 QTOQAEKHYEELLDQOKYDRLIEDYTKSNQKMEBEMQVLRGEHESIKDFIEHSK 709
 QY 344 DTPKKKRKRYSYGSLSPVSVSYLKTKPEQKV--ELOHISRCO-EDDTYVKONFYK 400
 Db 710 LTKQDLDKKNQFGIISSKRNQULSELEKSKLNSLALESKNNKKLENDLNLTEK 768
 QY 401 ETQETEKKLIFSEPIPHSPNLRGNEKRNKCSMLSTAEDIRONFT----QIPL 453
 Db 769 KNADIES---FRNTREALSKKALNDINGNINIIISDLNNKLSESTLQLOQNO 824
 QY 454 HKNKQECID-----SEHTLSENDELLERVHDYKC-NIQASVHVSDFSTDNSQ 503
 Db 825 DKNDIETLMERTSAADELSSMESINKNORNLAKQKCSNLQEKI-----NFGNK 876
 QY 504 -PKQKSDVLPFSKDK-----EKDHSIPTHDGLTINSQEHUTQVAKPFT 553
 Db 877 LAKSHTEKISSLEAKTAKTASTLSKELKTVKSENDLSLKVSNNDQ----- 925
 QY 554 PPEPNECDFKND-----SLPSKGKIH-KVKTLLRNKENLEPNAERDKRTEF 602
 Db 926 KEKSVNNEKFKEVSQLAENAEKNLARDEIEERLKVDIQJLONASLNMOSLKDNRIS 985
 QY 603 ITQEINR 609
 Db 986 DLESRNK 992

RESULT 12

RAFS—SCHPO
 ID YAFR—SCHPO; STANDARD; PRT; 1044 AA.
 AC Q00857; Q9P7V0; 1996-08-01 (Rel. 33, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE HYPOTHETICAL 119 kDa PROTEIN C29E6.03C IN CHROMOSOME 1.
 GN SPAC29E6.03C OR SPA29E6.03C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycotales; Schizosaccharomycetidae;
 OC Schizosaccharomyces.
 RN [1]
 RP SEQUENCE FROM N. A.
 RA STRAIN=972;
 RA Jones L., Murphy L., McNeil A., Simpson I., Harris D., Barrell B.G.,
 RA Rajandream M.A., Walsh S.V.;
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N. A.
 RC STRAIN=972;
 RA McDougall R.C., Rajandream M.A., Barrell B.G., Brown S., Murphy L.,
 RA Jones L., McNeil A., Harris D.,
 RA RESULT 13
 MYS3—SCHPO

Query Match 4.3%; Score 151.5; DB 1; Length 2104;
 Best Local Similarity 22.1%; Pred. No. 1.5;
 Matches 145; Conservative 112; Mismatches 242; Indels 157; Gaps 35;

QY 24 KNPLSLKSLKTDURPENSKC--KPLWKVFLDLPSPVTLSEKLOKDKIDGRVEEPLS 80
 QY ||:|| | |:|| -|| |:|| :||:|| :||:||

[1] MYS3_SCHPO STANDARD; PRT; 2104 AA.
 ID MYS3_SCHPO
 AC O41157; O42730;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE MYOSIN TYPE II HEAVY CHAIN 2.
 GN MYO3 OR MPP2 OR SPAC4A8.05C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1] SEQUENCE FROM N.A.
 RX MEDLINE=98119390; PubMed=9459302;
 RA Motegi F., Nakano K., Kitayama C., Yamamoto M., Mabuchi I.;
 RT "Identification of myo3, a second type-II myosin heavy chain in the
 fission yeast Schizosaccharomyces pombe.",
 FEMS Lett. 420:161-166(1997).
 RN [2] SEQUENCE FROM N.A.
 RX MEDLINE=98002346; PubMed=9398685;
 RA Baranilla M., Forsburg S.L., Pollard T.D.;
 RT "Identification of a second myo3-II in Schizosaccharomyces pombe:
 Myo2p is conditionally required for cytokinesis.,";
 Mol. Biol. Cell 8:2693-2705(1997).
 RN [3] SEQUENCE FROM N.A.
 RP STRAIN=72;
 RA Sletten J., Churcher C.M., Barrell B.G., Rajandream M.A., Wood V.;
 RL Submitted (AUG-1997) to the EMBL/Genbank/NCBI databases.
 CC -!- FUNCTION: STABILIZES THE F-ACTIN CABLES FORMING THE F-ACTIN RING
 THAT SURROUNDS THE NUCLEUS DURING INTERPHASE. MAY WORK IN
 CONJUNCTION WITH MYO2.
 CC -!- SURGENT: BINDS TO CDC4 AND RLC1.
 CC -!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
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 CC -----
 DR EMBL; AB007633; BAA24579.1; --.
 DR EMBL; AP029388; AAC04515.1; --.
 DR EMBL; Z98752; CAB14751; --.
 DR EMBL; P08799; IMND.
 DR InterPro; IPR001609; myosin_head.
 DR Pfam; PF00053; myosin_head_1.
 DR PRINTS; PRO0193; MYOSINHEAVY.
 DR PRODOM; PD000355; myosin_head; 1.
 DR SMART; SM00242; MYSC; 1.
 KW Myosin; Colled coil; Myp-binding; Actin-binding; Alkylation.
 FT DOMAIN 1 828 MYOSIN HEAD-LIKE.
 FT DOMAIN 2 104 COILED COIL (POTENTIAL).
 FT DOMAIN 646 660 ACTIN-BINDING (POTENTIAL).
 FT NIP_BIND 182 189 ATP (POTENTIAL).
 FT MOD_RES 686 686 ALKYLATION (BY SIMILARITY).
 FT CONFLICT 1193 1193 D -> G (IN REF. 2).
 FT CONFLICT 1304 1304 E -> G (IN REF. 2).
 FT CONFLICT 1344 1344 E -> K (IN REF. 2).
 FT CONFLICT 1420 1420 G -> D (IN REF. 2).
 SQ SEQUENCE 2104 AA; 242570 MW; 3A0548594028D258 CRC64;

RESULT 14
 ID MSP1_PLAC STANDARD; PRT; 1726 AA.
 AC P04934;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DE MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
 DE (PMMSA) (P195).
 GN MSP-1.
 OS Plasmodium falciparum (isolate Camp / Malaysia); Plasmodium.
 OC Eukaryota; Alveolata; Apicomplexa; Hemosporida; Plasmodium.
 OX NCBI_TaxID=5835;
 RN [1] SEQUENCE OF 1-1103 FROM N.A.
 RX MEDLINE=86205236; PubMed=3517809;
 RA Weber J.L., Leisinger W.M., Lyon J.A.;
 RT "Variation in the gene encoding a major merozoite surface antigen of
 the human malaria parasite Plasmodium falciparum.",
 Nucleic Acids Res. 16:206-206(1988).
 RN [2] SEQUENCE OF 1104-1726 FROM N.A.
 RX MEDLINE=88143999; PubMed=327299;
 RA Weber J.L., Sim B.K.L., Lyon J.A., Wolff R.;
 RT "Merozoite surface protein sequence from the Camp strain of the human
 malaria parasite Plasmodium falciparum.",
 Nucleic Acids Res. 16:206-206(1988).
 CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
 CC -!- PTM: MEROZOITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 42

Query Match	Score	DB 1	Length	1726
Best Local Similarity	20.4%	Prey	Nodes	14;
Matches	141;	Conservative	104;	Mismatches
Y	4.3%	Score 149.5;	DB 1;	Length 1726;
Y	65	QDKIDKJGGRVERE-----FLRDISYLISNEKEAQFTGPVSPSPESAYATTS	118	Best Local Similarity 20.4%; Prey, Nodes 14;
Y	309	QDLISINKQLERAHNLISVLKRDITL--KKNENIKELLDKIN-----EIKN	354	Matches 141; Conservative 104; Mismatches 224; Indels 223; Gaps 37;
Y	119	PPIPSHDSFQKPPDTVOLSRGKILV--EKAIDHDFIPSNSLNSNLSWMGWVILHID-D	174	355 PPPNSGN---TPNTL-LDKNRKIEEHEKIE-----IATKTFNISLFTDUPLE 401
Y	175	IRVYIEQKKEYLKKSTSVDGGKRVGSAQKTRGRLKKPFVQVEDMSOLYRPFYL	234	402 LEYVLRKNNKDVTPKSQDPPKS-----V 426
Y	235	QLTJNMPFINVSYSTQKPCSPFDV-----DKS--SMOKQVQKL--RQDGDK-----	277	427 QTPKVVPN-GIVYVPLPLTDINSLAADNDKNSYGDLMNPDTKEKINKEITDNDKTRKIF
Y	278	YCGTSIQLQLK--KKGICCECLOCYE---DLETHLISSEQHRNFAQSQNYQVDDI	330	486 INNIKKOILDEKKKINTKEQNKLLDYEKSKDVEELERFYEMKFNKNNDKWDVKI
Y	331	VKLVEDFVEYKEDTPKK-RTKYSGVSLSPSPASVLRKTGCKEKEKVLOHQSOKDQEDD	389	545 390 TTYKEQNFLYKETQET--EKKLIFISEPIPHNSNELRGLNEKMSNCKSMLSTAEDDIRON
Y	592	--ARYTYNEKQYRNKFSNNSNVQNLKKA-----LSYLEDYSLRKG-	591	447 546 FS-----AR
Y	592	--ISEKOPHNYTQTLKGLEADIKKLTBEEKIKSEN-----LEKN	629	591 390 TTYKEQNFLYKETQET--EKKLIFISEPIPHNSNELRGLNEKMSNCKSMLSTAEDDIRON
Y	448	FTQIQLPKHKNQCGILDSEHTSE-----NDLEELRVDHYRCNQIAHSVHVSDFSTDNS	500	629 592 --ISEKOPHNYTQTLKGLEADIKKLTBEEKIKSEN-----LEKN
Y	630	FKGITHSANASLEVYDVKLOVQVULLIKKIDIRKTEFLKNAQLKDSIHYVNPNIKQPN	689	629 448 FTQIQLPKHKNQCGILDSEHTSE-----NDLEELRVDHYRCNQIAHSVHVSDFSTDNS
Y	501	GSDP-----KOSDTV---LPAKDLIKEKD---LHST-----FTHDGLITNS	539	629 630 FKGITHSANASLEVYDVKLOVQVULLIKKIDIRKTEFLKNAQLKDSIHYVNPNIKQPN
Y	690	KPEPYYLTVLKVKEVDKLFKEFTRKVDMLKKEAOVLLSITQPLVAASETTEDGCHSTHMLS	749	629 501 GSDP-----KOSDTV---LPAKDLIKEKD---LHST-----FTHDGLITNS
Y	540	Q-----EHLTVOAKAPHT-----PPEE-----PNEDCDRKNMDSLPSGKIHRYVKII	581	629 690 KPEPYYLTVLKVKEVDKLFKEFTRKVDMLKKEAOVLLSITQPLVAASETTEDGCHSTHMLS
Y	750	QSGETEYETEETETEETEVGHTT-----TITLPPKVWVNSIEJKSNND-----	796	629 540 Q-----EHLTVOAKAPHT-----PPEE-----PNEDCDRKNMDSLPSGKIHRYVKII
Y	582	LGRNRKENLEPNAEFDKTRTEOENRIC-----SSPVQSLDIFQ-TSEEKSEFL	632	629 750 QSGETEYETEETETEETEVGHTT-----TITLPPKVWVNSIEJKSNND-----
Y	797	-----SOALTKVYVLLKLDDEFIL--KSYCHRYLIVNSNSMDOKLLEVNVNLTPEEEENL-	848	629 582 LGRNRKENLEPNAEFDKTRTEOENRIC-----SSPVQSLDIFQ-TSEEKSEFL
Y	633	GFTSYTKEKGICINVLDIWEENEDNLITAFFS	664	629 797 -----SOALTKVYVLLKLDDEFIL--KSYCHRYLIVNSNSMDOKLLEVNVNLTPEEEENL-
Y	849	-----KS---CDPLDL--ENLONNIPAMYS	869	629 633 GFTSYTKEKGICINVLDIWEENEDNLITAFFS

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